

## SEQUENCE LISTING

<110> Harding, Robert Maxwell  
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 Becker, Douglas Keith  
 Hafner, Gregory John  
 Yang, Ilin

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<210> 3
<211> 146
<212> PRT
<213> Taro bacilliform virus

<400> 3

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Met Ala Lys Lys Phe Glu Ala Ala Ile Lys Asp Trp Tyr Asp Asn Ser  
1 5 10 15

Arg Arg Ala Asp Leu Ser Tyr Leu Asp Leu Ala Thr Thr Thr Lys Pro  
20 25 30

Ser Ala Ser Gln Leu Ala His Asn Leu Gln Val Ile Phe Asp Arg Leu  
35 40 45

Ser Leu His Ser Ser Val Ser Ile Lys Glu His Tyr Glu Val Val Ser  
50 55 60

Lys Leu His Ser Leu Glu Lys Ser Ile Glu Glu Leu Lys Ser Glu Leu  
65 70 75 80

Thr Thr Val Lys Arg Ala Leu Thr Ser Ile Gln Lys Glu Val Phe Thr  
85 90 95

His Lys Pro Leu Thr Ala Gln Glu Val Gln Thr Leu Ala Gln Ser Leu  
100 105 110

Ile Lys Glu Pro Lys Gln Ile Glu Gln Gln Ala Val Phe Leu Leu Lys  
115 120 125

Glu Leu Lys Glu Gln Thr Ala Lys Ile Gln Ala Leu Leu His Glu Leu  
130 135 140

Lys Ser  
145

<210> 4  
<211> 144  
<212> PRT  
<213> Taro bacilliiform virus

<400> 4

Met Ser Val Pro Asn Ser Thr Tyr Pro Gly Tyr Ile Lys Ser Leu Glu  
1 5 10 15

Glu Thr Lys Val Leu Gly Asp Pro Ser Val Gly Phe Ser Glu Ile Pro  
20 25 30

Thr Thr Ala Ile Gly Thr Ala Thr Gly Phe Ser Thr Leu Tyr Lys Gln  
35 40 45

Asn Asn Thr Ile Ile Asn Leu Leu Ile Ser Leu His Lys Lys Val Asp  
50 55 60

Ser Leu Ser Lys Lys Thr Asp Val Asp Glu Leu Ala Thr Glu Leu Ser  
65 70 75 80

Lys Leu Thr Ile Lys Asp Thr Pro Lys Val Lys Ala Lys Thr Pro Leu  
85 90 95

Tyr Val Phe Lys Ser Pro Arg Leu Ile Leu Glu Glu Glu Arg Tyr Lys  
100 105 110

Ile Gly Leu Pro Pro Thr Thr Thr Asp Trp Thr Trp Pro Val Gly His  
115 120 125

Pro Phe Ala Pro Pro Pro Lys Thr Ser Thr Lys Ala Ser Thr Ser Ser  
130 135 140

<210> 5  
<211> 1881  
<212> PRT  
<213> Taro bacilliiform virus

<400> 5

Met Ser Leu Ala Val Arg Asp Arg Gly Ser Asn Pro Ser Thr Ser Ser  
1 5 10 15

Thr Val Pro Ser Gln Gln Asp Gln Ile Arg Asp Tyr Arg Asn Met Gln  
20 25 30

Arg Val Arg His Thr Ala Glu Arg Ala Ala Arg Arg Ile Phe Pro Gly  
35 40 45

Arg Phe Asn Arg Thr Leu Glu Ser Gln Ile Asn Pro Glu Ala Glu Ile  
50 55 60

Arg Leu Ser Gln Gln Arg Arg Ala Ala Met Val Pro Ala Glu Val Leu  
65 70 75 80

Tyr Asn Thr Ser Pro Ser Thr Arg Asn Gln Lys Val Tyr Gln His Tyr  
85 90 95

Ser Glu Glu Arg Ile Leu Cys Thr Gly Gln Asn Gln Gln Leu Asn Leu  
 100 105 110

Pro Phe Ile Asn Glu Ser Ser Tyr Arg Ala Leu Arg Glu Ser Gly Gln  
 115 120 125

Gln His Leu His Ile Gly Leu Ile Met Ile Arg Val His Pro Leu His  
 130 135 140

Arg Arg Asn Ala Gly Thr Thr Ala Leu Ile Val Pro Arg Asp Ile Arg  
 145 150 155 160

Trp Asn Asp Asp Arg Ser Ile Ile Gly Thr Met Glu Ile Asp Leu Ser  
 165 170 175

Ala Gly Ser Gln Ile Val Tyr Ile Ala Pro Asn Ile Met Leu Ser Val  
 180 185 190

Glu Asp Phe Tyr Arg Asn Ile Gln Leu Ala Ile Gln Thr Gln Gly Tyr  
 195 200 205

Glu Asn Trp Asn Ser Ala Glu Ser Asn Leu Leu Ile Ser Arg Ala Leu  
 210 215 220

Ile Gly Arg Leu Thr Asn Asp Ser Phe Thr Gly Phe Gln Tyr Asn Ile  
 225 230 235 240

Ser Asn Val Ala Glu Tyr Leu His Ser His Gly Val Gln Ala Ile Glu  
 245 250 255

Gly Gln Ala His Pro Arg Thr Leu Gly Asn Arg Trp Ile Leu Gln Ala  
 260 265 270

Pro Ala Pro Pro Arg Ser Leu Val Pro Gln Asn Val Glu Thr Thr Thr  
 275 280 285

Leu Leu Asp Gly Asn Val Ser Ile Arg Phe Ser Asn Tyr His Gln Ala  
 290 295 300

Pro Val Asn Asp Thr Gln Asp Asn Ser His Pro Asp Ile Gln Glu Asp  
 305 310 315 320

Glu Asn Gln Phe Ile Gly Phe Leu Ser Asp Leu Gly Glu Glu Tyr Glu

325										330					335				
Leu	Glu	Tyr	Pro	Ser	Phe	Thr	Pro	Val	His	Ala	Asp	Glu	Phe	Ile	Phe				
			340					345					350						
Ile	Ile	Ile	Asn	Gly	Glu	Glu	Ile	Pro	Asp	Asp	Phe	Val	Ser	Ser	Phe				
		355					360					365							
Cys	Ser	Asn	Phe	Ser	Pro	Pro	Pro	Ile	Pro	Glu	Pro	Glu	Pro	Thr	Ala				
	370					375					380								
Ile	Glu	Glu	Thr	Ala	Phe	Thr	Leu	Glu	Glu	Gln	Phe	Asn	Asp	Leu	Asp				
385					390					395					400				
Tyr	Pro	Thr	Leu	Ile	Ser	Met	Glu	Lys	Gln	Leu	Val	Gln	Ser	Ser	Val				
				405					410						415				
Thr	Ser	Ala	Tyr	Asn	Pro	Pro	Thr	Glu	Pro	Leu	Met	Gly	Gln	Val	Val				
			420					425					430						
Tyr	Pro	Pro	Ala	Ser	Ala	Pro	Arg	Pro	Gln	Ala	Glu	Thr	Ser	Ser	Thr				
		435					440					445							
Ser	Glu	Arg	Phe	Lys	Asn	Phe	Arg	Ala	Lys	Pro	Tyr	Ser	Thr	Pro	Thr				
	450					455					460								
Ile	Phe	Leu	Pro	Pro	Ala	Tyr	Asn	Gln	Gln	Gly	Ala	Ile	Leu	Val	Leu				
465					470					475					480				
Pro	Asp	Asp	Ile	Gly	Leu	Tyr	Glu	Asp	Thr	Ile	Ser	Arg	Trp	Glu	Ser				
				485					490					495					
Ile	Thr	Leu	Asn	Met	Met	Asn	Glu	Lys	Val	Trp	Pro	Ser	Asn	Glu	Ala				
			500					505					510						
Lys	Ala	Lys	Tyr	Met	Glu	Asn	Leu	Leu	Gly	Glu	Met	Glu	Lys	Lys	Thr				
		515					520					525							
Trp	Ile	Gln	Trp	Arg	Thr	Thr	Tyr	Val	Ser	Glu	Tyr	Asp	Ala	Leu	Val				
	530					535					540								
Gln	Gln	Ser	Asp	Glu	Thr	Gln	Asn	Leu	Leu	Ser	Gln	Val	Arg	Arg	Ile				
545					550					555					560				

Phe Leu Leu Gln Asp Pro Tyr Gln Gly Ser Thr Ala Glu Gln Asp Gln  
 565 570 575

Ala Tyr Asn Asp Leu Glu Arg Ile Ser Cys Asp Asn Ile Lys Asp Leu  
 580 585 590

Ile Pro Tyr Leu Ile Gln Phe Arg Asn Leu Ala Ala Lys Ser Gly Arg  
 595 600 605

Leu Phe Leu Gly Pro Glu Leu Ser Glu Lys Leu Phe Arg Lys Met Pro  
 610 615 620

Pro Leu Ile Gly Lys Glu Ile Glu Thr Ala Phe Ile Ala Lys His Gly  
 625 630 635 640

Asn Ala Asn Ile Thr Val Met Pro Arg Ile His Phe Ala Tyr His Tyr  
 645 650 655

Leu Ala Glu Leu Cys Lys Lys Ala Ala Leu Gln Arg Ser Leu Lys Asp  
 660 665 670

Leu Ser Phe Cys Asn Gln Ile Pro Leu Pro Gly Ile Tyr Thr Lys Gly  
 675 680 685

Asn Lys Lys Phe Gly Leu Arg Lys Ala Arg Thr Tyr Lys Gly Lys Pro  
 690 695 700

His Pro Thr His Val Arg Val Phe Lys Lys Ala Lys Tyr Gln Arg Thr  
 705 710 715 720

Lys Lys Cys Lys Cys Phe Ile Cys Gly Glu Pro Gly His Phe Ala Arg  
 725 730 735

Glu Cys Thr Lys Gln Arg Gly Asn Ile Val Arg Ala Thr Val His Gln  
 740 745 750

Glu Leu Ala Ile Pro Asp Asn Phe Asp Val Val Ser Val Asp Ala Asp  
 755 760 765

Glu Ser Asp Ser Ser Gly Ile Tyr Ser Tyr Ser Glu Asn Glu Ala Pro  
 770 775 780

Leu Gln Glu Val Asn Ser Phe Ile His Asp Glu Asn Ile Phe Phe Leu  
785 790 795 800

Ser Asp Ala Asp Glu Phe Glu Ser Pro Gln Gln His Leu His Glu Thr  
805 810 815

Val Asn Met Leu Gln Ser Arg Ser Ala Tyr Leu Pro Gln Val Ala Val  
820 825 830

Gly Glu Glu Lys Leu Asn Cys Ser His Ile Trp Leu Gln Asp Val Asp  
835 840 845

Ile Pro Ser Asp Lys His Lys Cys His Thr Cys Arg Arg Asp Thr Gln  
850 855 860

Lys His Tyr Arg Leu Glu Cys Gln Lys Cys Lys Phe Leu Val Cys Ser  
865 870 875 880

Leu Cys Thr Ile Pro Tyr Leu Gly Ile Thr Met Gln Phe Arg Gln Lys  
885 890 895

Gln Lys Ser Gln Pro Glu Asn Pro Asn Leu Val Arg Glu Leu Leu Glu  
900 905 910

His Ala Ile Phe Leu Glu Glu Lys Cys Lys Asn Gln Glu Leu Leu Ser  
915 920 925

Glu Thr Gln Ile Glu Arg Ile Val Ser Ser Glu Lys Gln Val Lys Phe  
930 935 940

Tyr Gly Ile Leu Pro Thr Lys Lys Ser Asn Lys Ser Ala Gly Tyr Asp  
945 950 955 960

Leu Gln Ser Asn Ile Asp Ile Glu Ile Pro Pro Gly Lys Cys Thr Val  
965 970 975

Ile Ser Thr Gly Thr Phe Leu Gln Met Pro Asp Asn Met Tyr Gly Arg  
980 985 990

Leu Val Glu Arg Thr Ser Leu Ala Ile Gln Gly Ile Thr Val Gln Gly  
995 1000 1005

Gly Val 1010	Ile Asp Pro Asp Phe 1015	Thr Gly Glu Ile Gln 1020	Ile Val Leu
Phe Asn 1025	His Asn Thr Ala Pro 1030	Tyr Pro Val Lys Lys 1035	Thr Tyr Arg
Leu Ala 1040	Gln Ile Ile Phe Glu 1045	Lys Phe Tyr Thr Pro 1050	Ile Phe Ile
Gln Glu 1055	Pro Phe Thr Ser Thr 1060	Gln Gln Gly Ser Ser 1065	Asn Phe Gly
Ser Thr 1070	Ala Lys Pro Leu Gln 1075	Ile Thr Glu Asn Ile 1080	Glu Val Met
Ser Glu 1085	Thr Val Ala Asn Gln 1090	Val Ala Lys Ser Ser 1095	Val Leu Pro
Arg Leu 1100	Tyr Ser Ile Gln Ala 1105	His Ile His Ile Ala 1110	Pro Asp Ile
Val Ile 1115	Ser Thr Thr Ala Ile 1120	Ile Asp Thr Gly Ala 1125	Thr Val Cys
Cys Ile 1130	Ser Glu Lys Ile Val 1135	Pro Glu Ala Ala Lys 1140	Glu Gln Leu
Asn Tyr 1145	Lys Val Asn Ile Ser 1150	Gly Ile Ser Ser Gln 1155	Gln Gln Ile
Gln His 1160	Arg Leu Lys Arg Gly 1165	Thr Leu Glu Ile Ala 1170	Ser Asn Lys
Tyr Ala 1175	Leu Pro Leu Cys Tyr 1180	Ile Ile Glu Leu Asn 1185	Asp Lys Asp
Asp Phe 1190	Ser Met Ile Leu Gly 1195	Cys Asn Phe Phe Lys 1200	His Met Gly
Gly Gly 1205	Met Arg Phe Glu Gly 1210	Pro His Val Thr Phe 1215	Tyr Lys Gly
Ile Thr	Thr Leu Ser Thr Ser	Tyr Ala Asn Thr Gly	Ile Asp Thr



1220		1225		1230
Glu His	Glu Gln Ile Thr	Ser Thr Thr Ser Gln	Ser Phe Lys Glu	
1235		1240	1245	
Arg Phe	Ser Pro Leu Met	Asn Glu Leu Lys Ala	Ala Gly Tyr Ile	
1250		1255	1260	
Gly Glu	Asp Pro Leu Lys	His Trp Ser Lys Asn	Lys Val Thr Cys	
1265		1270	1275	
Lys Leu	Asp Leu Lys Asn	Thr Glu Ile Thr Ile	Gln Asp Lys Pro	
1280		1285	1290	
Leu Arg	His Ile Thr Pro	Ala Leu Glu Gln Ser	Tyr Gly Arg His	
1295		1300	1305	
Val Asn	Ala Leu Leu Met	Leu Lys Val Ile Gln	Pro Ser Lys Ser	
1310		1315	1320	
Arg His	Arg Thr Met Ala	Phe Leu Val Asn Ser	Gly Thr Thr Val	
1325		1330	1335	
Thr Ala	Asp Gly Lys Glu	Ile Lys Gly Lys Glu	Arg Met Val Phe	
1340		1345	1350	
Asn Tyr	Lys Ala Leu Asn	Asp Asn Thr Tyr Lys	Asp Gln Tyr Ser	
1355		1360	1365	
Leu Pro	Asn Ile Gln Leu	Ile Leu Lys Lys Val	Ile Asn Ser Thr	
1370		1375	1380	
Ile Tyr	Ser Lys Phe Asp	Leu Lys Ser Gly Phe	His Gln Val Ala	
1385		1390	1395	
Met Asp	Pro Asp Ser Val	Glu Trp Thr Ala Phe	Leu Val Pro Gln	
1400		1405	1410	
Gly Leu	Tyr Glu Trp Leu	Ala Met Pro Phe Gly	Leu Lys Asn Ala	
1415		1420	1425	
Pro Ala	Val Phe Gln Arg	Lys Met Asp Ala Val	Phe Lys Gly Cys	
1430		1435	1440	

Glu	Lys	Phe	Leu	Ala	Val	Tyr	Ile	Asp	Asp	Ile	Leu	Val	Phe	Ser
1445						1450					1455			
Asn	Asn	Glu	Glu	Asp	His	Ala	Lys	His	Leu	Val	Ile	Met	Leu	Gln
1460						1465					1470			
Arg	Cys	Lys	Glu	His	Gly	Leu	Val	Leu	Ser	Pro	Thr	Lys	Met	Asn
1475						1480					1485			
Ile	Ala	Val	Arg	Glu	Val	Asn	Phe	Leu	Gly	Ala	Thr	Ile	Gly	Ser
1490						1495					1500			
Arg	Lys	Val	Lys	Leu	Gln	Glu	Asn	Ile	Ile	Lys	Lys	Ile	Leu	Asp
1505						1510					1515			
Phe	Asp	Thr	Glu	Lys	Leu	Gln	Ser	Lys	Lys	Gly	Leu	Arg	Ser	Phe
1520						1525					1530			
Leu	Gly	Ile	Leu	Asn	Tyr	Ala	Arg	Asn	His	Ile	Pro	Asn	Leu	Gly
1535						1540					1545			
Lys	Ile	Ala	Gly	Pro	Leu	Tyr	Ser	Lys	Thr	Ser	Ile	Tyr	Gly	Asp
1550						1555					1560			
Ile	Arg	Phe	Ser	Ala	Ser	Asp	Trp	Lys	Leu	Ile	Asn	Glu	Ile	Lys
1565						1570					1575			
Ala	Ile	Val	Glu	Lys	Leu	Pro	Pro	Leu	Asp	Tyr	Pro	Pro	Glu	Gln
1580						1585					1590			
Ala	Tyr	Ile	Ile	Ile	Glu	Ser	Asp	Gly	Cys	Met	Glu	Gly	Trp	Gly
1595						1600					1605			
Ala	Ile	Cys	Lys	Trp	Lys	Leu	Ala	Glu	Tyr	Asp	Pro	Lys	Ser	Ser
1610						1615					1620			
Glu	Gln	Ile	Cys	Ala	Tyr	Ala	Ser	Gly	Lys	Phe	Ser	Pro	Ile	Lys
1625						1630					1635			
Ser	Thr	Ile	Asp	Ala	Glu	Ile	Thr	Ala	Ala	Met	Glu	Gly	Leu	Glu
1640						1645					1650			

Ala Phe Lys Ile His Tyr Leu Asp Lys Gln Lys Ile Thr Leu Arg  
 1655 1660 1665

Thr Asp Cys Gln Ala Ile Ile Ser Phe Cys Asn Lys Thr Ser Val  
 1670 1675 1680

Asn Lys Pro Ser Arg Val Arg Trp Leu Lys Phe Ile Asp Tyr Ile  
 1685 1690 1695

Thr Asn Thr Gly Ile Asp Val Lys Phe Glu His Ile Asp Ala Lys  
 1700 1705 1710

Asn Asn Val Leu Ala Asp Thr Leu Ser Arg Leu Val Asn Thr Leu  
 1715 1720 1725

Gln Asp Leu Pro Trp Leu Asp Glu Pro His Gln Asp Gln Thr Val  
 1730 1735 1740

Ser Leu Met Gln Glu Ile Glu Asp Ala Pro Leu Glu Ile Lys Gln  
 1745 1750 1755

Arg Ser Leu Thr Cys Leu Gln Arg Leu Ile Cys Arg Ser Phe Met  
 1760 1765 1770

Glu Asp Ser Thr Glu Glu Ala Ile His Phe Leu Glu Asp Asp Lys  
 1775 1780 1785

Ile Glu Pro Thr Ala Glu Ser Ser Thr Pro Ile Thr Leu Asp Glu  
 1790 1795 1800

Phe Ser Arg Lys Arg Phe Gln Glu His Thr Asp Leu Leu Glu Glu  
 1805 1810 1815

Phe Gln Leu Thr Leu Leu Gln Ile Asn Leu Leu Glu Ala Ser Leu  
 1820 1825 1830

His Glu Arg Leu Met Lys Cys Gln Ser Tyr Ala Thr Arg Asp Asn  
 1835 1840 1845

Phe Trp Gly Asp Trp Leu Pro Glu Ala Arg Arg Asp Leu Leu Gln  
 1850 1855 1860

Ile Gln Leu Ala Lys Glu Ile Ile Glu Lys Val Arg Glu Lys Leu  
 1865 1870 1875

His Ser Ile  
 1880

<210> 6  
 <211> 1190  
 <212> DNA  
 <213> Taro bacilliform virus

<400> 6  
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 taaatttgaa catattgatg ctaaaaataa tgtcttagct gacactctgt ccagggttagt 120  
 taacactttg caggatttgc catggctaga tgaacctcat caggatcaaa cagtctccct 180  
 gatgcaggaa attgaagatg cacctcttga aatcaagcag cgttctttaa cctgcttaca 240  
 gagactgatc tgtagaagct tcatggaaga ttctacagaa gaagctattc acttcctcga 300  
 agatgataag atcgagccaa cagctgagtc atcaacccca attactttgg atgaattttc 360  
 aagaaaaaga ttccaagaac atacagatct cttagaagaa tttcaattaa ctttgcttca 420  
 aattaatctt cttgaagcat ctcttcatga acgattaatg aaatgccaaa gttatgcaac 480  
 gagagataat ttctggggag attggctgcc tgaagctcgc agagatcttt tgcaaattca 540  
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 ctttgtgtgt gagtggcgca cttgcgcata atgtagtaag gaattattgt actttttacgc 660  
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 ggggagccgt tcgtacaaag tagatgcttt tctagtcaca tctgactttt ctaaaagcag 780  
 atgccatcaa ctttattcga gttgagcctc ggggagccgc tcgttttaaag atgctctttt 840  
 gaaaatgaca gcgcgtgggt cgatgtcatt ctcacctttt ctttaaatgcg tcggccaccg 900  
 actgcattat tgagattctc ttatcccttt gccacctcat cggttgcatt attgggattt 960  
 cgtatcgagt cgagggacga ggcctccact actcctataa aaggacctca acccctcaga 1020  
 agaacggcaa gccggaaaca ccgaacttcc cattcttctc ttgagtcttt cttttgagct 1080  
 tgagcttgtg tgtaatcttt catagtttct aagtctccga agaacgagca ccgtctcgtg 1140  
 aaggagccga tcctttttcca accacacttt ttctaccttg gtatcagagc 1190

<210> 7  
 <211> 598

&lt;212&gt; DNA

&lt;213&gt; Taro bacilliform virus

&lt;400&gt; 7

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ttttacgctg gacgccacta ggctccatgc tttctgtaat gtcacatcac ttttacgaat      120
tgagcctcgg ggagccgttc gtacaaagta gatgcttttc tagtcacatc tgacttttct      180
aaaagcagat gccatcaact ttattcgagt tgagcctcgg ggagccgctc gtttaaagat      240
gctcttttga aaatgacagc gcgtgggtgcg atgtcattct caccttttct ttaatgcgtc      300
ggccaccgac tgcattattg agattctctt atccctttgc cacctcatcg gttgcattat      360
tgggatttcg tatcgagtcg agggacgagg cctccactac tcctataaaa ggacctcaac      420
ccctcagaag aacggcaagc cggaaacacc gaacttccca ttcttctctt gagtctttcc      480
tttgagcttg agcttgtgtg taatctttca tagtttctaa gtctccgaag aacgagcacc      540
gtctcgtgaa ggagccgac cttttccaac cacacttttt ctaccttggt atcagagc      598

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&lt;210&gt; 8

&lt;211&gt; 529

&lt;212&gt; DNA

&lt;213&gt; Taro bacilliform virus

&lt;400&gt; 8

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ggagcgccact aggctccatg ctttctgtaa tgtcacatca cttttacgaa ttgagcctcg      60
gggagccggt cgtacaaagt agatgctttt ctagtcacat ctgacttttc taaaagcaga      120
tgccatcaac tttattcgag ttgagcctcg gggagccgct cgtttaaaga tgctcttttg      180
aaaatgacag cgcgtgggtgc gatgtcattc tcaccttttc tttaatgcgt cggccaccga      240
ctgcattatt gagattctct tatccctttg ccacctcatc gggtgcatta ttgggatttc      300
gtatcgagtc gagggacgag gcctccacta ctctataaaa aggacctcaa ccctcagaa      360
gaacggcaag ccggaaacac cgaacttccc attcttctct tgagtctttc ctttgagctt      420
gagcttgtgt gtaatctttc atagtttcta agtctccgaa gaacgagcac cgtctcgtga      480
aggagccgat ctttttccaa ccacactttt tctaccttgg tatcagagc      529

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&lt;210&gt; 9

&lt;211&gt; 261

&lt;212&gt; DNA

&lt;213&gt; Taro bacilliform virus

&lt;400&gt; 9

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tgccacctca tcggttgcat tattgggatt tcgtatcgag tcgagggacg aggcctccac      60

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tactcctata aaaggacctc aaccctcag aagaacggca agccggaaac accgaacttc      120
ccattcttct cttgagtctt tcctttgagc ttgagcttgt gtgtaatctt tcatagtttc      180
taagtctccg aagaacgagc accgtctcgt gaaggagccg atccttttcc aaccacactt      240
tttctacctt ggtatcagag c                                                  261
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<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence
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<220>
<223> Badna FP primer
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<220>
<221> modified_base
<222> (5)..(6)
<223> I
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<220>
<221> modified_base
<222> (10)..(11)
<223> I
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<220>
<221> modified_base
<222> (18)..(19)
<223> I
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<400> 10
atgccttygg aaraaygcc      20
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```
<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence
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<220>
<223> Badna RP primer
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<220>
<221> modified_base
<222> (9)..(10)
<223> I
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<220>
<221> modified_base
<222> (11)..(12)
<223> I
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<220>  
<221> modified\_base  
<222> (13)..(14)  
<223> I

<220>  
<221> modified\_base  
<222> (18)..(19)  
<223> I

<400> 11  
ccayttrcaa csc-----cacc 20

<210> 12  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 1F primer

<400> 12  
ggatgcagta ttcaaagggt gtg 23

<210> 13  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> TRBR primer

<400> 13  
ctgcaggcgg ccgcgctctg atacca 26

<210> 14  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5F primer

<400> 14  
agtctttcct ttgagcttga gc 22

<210> 15  
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